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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=27; hr=14; min=5; sec=52; ms=114; ]

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Application No: 10589180 Version No: 1.0

**Input Set:**

**Output Set:**

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**Finished:** 2008-08-23 06:13:33.279  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 232 ms  
**Total Warnings:** 49  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 54  
**Actual SeqID Count:** 54

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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (21)
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W 213	Artificial or Unknown found in <213> in SEQ ID (24)
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**Input Set:**

**Output Set:**

**Started:** 2008-08-23 06:13:30.047  
**Finished:** 2008-08-23 06:13:33.279  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 232 ms  
**Total Warnings:** 49  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 54  
**Actual SeqID Count:** 54

Error code	Error Description
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SEQUENCE LISTING

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LaMonica, Nicola  
Facciabene, Andrea  
Aurisicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND  
USES THEREOF

<130> ITR0073YP

<140> 10589180  
<141> 2008-08-23

<150> PCT/EP2005/001114  
<151> 2005-02-03

<150> 60/635,791  
<151> 2004-12-14

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<160> 54

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<223> PCR Primer, chemically synthesized

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<223> CEA-LTA fusion

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acggccgttca atgtcgacaa ggggaaggag gtgcTTCTAC ttgtccacaa tctgccccag 180  
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accctacacg tcataaaagtc agatcttgg aatgaagaag caactggcca gttccgggtta 420  
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480

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 <211> 921  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CEA-LTB fusion

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 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly  
 35 40 45  
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly  
 50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile  
65 70 75 80  
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser  
85 90 95  
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile  
100 105 110  
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp  
115 120 125  
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu  
130 135 140  
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys  
145 150 155 160  
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr  
165 170 175  
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln  
180 185 190  
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn  
195 200 205  
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg  
210 215 220  
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro  
225 230 235 240  
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn  
245 250 255  
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe  
260 265 270  
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn  
275 280 285  
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser  
290 295 300  
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala  
305 310 315 320  
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu  
325 330 335  
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr  
340 345 350  
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg  
355 360 365  
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr  
370 375 380  
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser  
385 390 395 400  
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp  
405 410 415  
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn  
420 425 430  
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser  
435 440 445  
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile  
450 455 460  
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn  
465 470 475 480  
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val  
485 490 495  
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro  
500 505 510  
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln

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Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
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Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
595	600	605	
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln			
610	615	620	
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
625	630	635	640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
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Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
660	665	670	
Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg			
675	680	685	
Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met			
690	695	700	
Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile			
705	710	715	720
Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr			
725	730	735	
Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu			
740	745	750	
Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val			
755	760	765	
Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val			
770	775	780	
Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile			
785	790	795	800
Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile			
805	810	815	
Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg			
820	825	830	
Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe			
835	840	845	
Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala			
850	855	860	
Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys			
865	870	875	880
Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln			
885	890	895	
Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser Glu Val Asp			
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Ile Tyr Asn Arg Ile Arg Asp Glu Leu			
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<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

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<210> 10

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

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35 40 45  
Lys Glu Val Leu Leu Leu His Asn Leu Pro Gln His Leu Phe Gly  
50 55 60  
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile  
65 70 75 80  
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser  
85 90 95  
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile  
100 105 110  
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp  
115 120 125  
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu  
130 135 140  
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys  
145 150 155 160  
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr  
165 170 175  
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln  
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Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg  
210 215 220  
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro  
225 230 235 240  
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn  
245 25